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<110> Gozes, Illana
Brenneman, Douglas E.
Bassan, Merav
Zamostiano, Rachel
The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services

<120> Activity Dependent Neurotrophic Factor III (ADNF III)

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<141> 1998-11-06

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<151> 1997-02-07

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<170> PatentIn Ver. 2.0

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Ser Gln Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala
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 gaagggtttt ggtccaagga ccagtcacag tggaaaatg catctgagaa tgcagagcgc 2280
 ttaccaaacc cacagattga gtggcagaat agcacaattt acagttagga cggggagcag 2340
 tttgacagca tgactgacgg agttgctgat cccatgcattt gcagcttaac tggagtgaag 2400

ctgagcagcc agcaaggctg a 2421

<210> 5
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF-9 active peptide antigen

<400> 5
 Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5

<210> 6
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF III-8 active site core peptide, clone 25 sequence (NAP)

<400> 6
 Asn Ala Pro Val Ser Ile Pro Gln
 1 5

<210> 7
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense primer for amplification of ADNF III cDNA

<400> 7
 tccaaatgttc acctgcag 18

<210> 8
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense primer (bases 438-455) for amplification of ADNF III cDNA

<400> 8
 gctcggttaca gattgtac 18

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense primer
 (bases 71-90) for amplification of ADNF III cDNA

<400> 9
 acctgcagca aaacaactat 20

<210> 10
 <211> 88
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:activity
 dependent neurotrophic factor III (ADNF III)
 polypeptide

<220>
 <221> MOD_RES
 <222> (1)..(40)
 <223> Xaa = any amino acid, Xaa at positions 1-40 may be
 present or absent

<220>
 <221> MOD_RES
 <222> (49)..(88)
 <223> Xaa = any amino acid, Xaa at positions 49-88 may be
 present or absent

<400> 10
 Xaa
 1 5 10 15

Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Ala Pro Val Ser Ile Pro Gln
 35 40 45

Xaa
 50 55 60

Xaa
 65 70 75 80

Xaa
 85

<210> 11
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:short hsp60
homolog control peptide

<400> 11
Leu Gly Gly Gly Ser
1 5

<210> 12
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 12
Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln
1 5 10 15
Gln Ser

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF III
polypeptide; short hsp60 homolog control peptide

<400> 13
Val Leu Gly Gly Gly
1 5

<210> 14
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 14
Val Leu Gly Gly
1

<210> 15
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 15
Val Leu Gly Gly Val
1 5

<210> 16
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 16
Gly Val Leu Gly Gly
1 5

<210> 17
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 17
Leu Gly Leu Gly Gly
1 5

<210> 18
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 18
Ser Val Arg Leu Gly Leu Gly Gly
1 5

<210> 19
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:related to
yeast protein PIF1

<220>
 <221> MOD_RES
 <222> (7)
 <223> Xaa = unknown

<220>
 <221> MOD_RES
 <222> (10)
 <223> Xaa = unknown

<400> 19
 Pro Gln Leu Ile Ser Glu Xaa Ser Phe Xaa Gln
 1 5 10

<210> 20
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:related to
 yeast protein PIF1

<220>
 <221> MOD_RES
 <222> (5)
 <223> Xaa = unknown

<220>
 <221> MOD_RES
 <222> (8)
 <223> Xaa = unknown

<220>
 <221> MOD_RES
 <222> (10)
 <223> Xaa = unknown

<400> 20
 Ile Gln Leu Glu Xaa Glu Ile Xaa Glu Xaa Gln Ile Ile
 1 5 10

<210> 21
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF
 I/hsp60-related sequence conjugated through the
 Cys residue to Sephadex for affinity
 chromatography

<400> 21
 Cys Val Leu Gly Gly Gly Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5 10 15

<210> 22
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:peptide
 conjugated through the Cys residue to Sephadex for
 affinity chromatography

<400> 22
 Cys Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5 10

<210> 23
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:active peptide
 of ADNF I hsp60-related sequence

<400> 23
 Val Leu Gly Gly Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5 10

<210> 24
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hsp60 homolog
 peptide

<400> 24
 Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala
 1 5 10

<210> 25
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mimic hybrid
 primer

<400> 25
 acctgcagca aaacaactat tttccatccc tcaacagt

38

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:cyclophilin
 mRNA upper primer, position 348

<400> 26
 atggcacagc aggaaagagc

20

<210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:cyclophilin
 mRNA lower primer

<400> 27
 ttgccggagt cgacaatgat

20

<210> 28
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sequence of p25
 clone with structural similarity to active peptide
 of ADNF I

<400> 28
 Gly Gly Asn Ala Pro Val Ser Ile Pro
 1 5

<210> 29
 <211> 837
 <212> DNA
 <213> Homo sapiens

<220>
 <223> PCR of human ADNF III cDNA from human
 neuroblastoma, sense

<400> 29
 cattggggccg acgtcgcatg ctcccgccg ccatggccgc gggattacct gcagcaaaac 60
 aactatggag tcaaattctgt aggccagggc tacagtgttg gtcagtcatt gagactgggt 120
 ctaggtggca acgcaccagt ttccattcct caacaatctc agtctgtaaa gcagttactt 180
 ccaagtggaa acggaaggc ttatggctt gggtcagagc agaggtccca ggcaccagca 240
 agatactccc tgcagtctgc taatgcctct tctctctcat cggggccagtt aaagtctcct 300
 tccctctctc agtcacaggc atccagagtg ttaggtcagt ccagttccaa acctgctgca 360
 gctgccacag gccctccccc aggttaacact tcctcaactc aaaagtggaa aatatgtaca 420
 atctgttaacg agcaatcaact agtgccggccg cctgcaggc gaccatatgg gagagctccc 480

aacgcgttgg atgcatacg ttagtattct atagtgtcac ctaaatagct tggcgtaatc 540
 atggtcatacg ctgtttcctg tgtgaaattg ttatccgctc acaattccac acaacatacg 600
 aaccggaagc ataaagtgt aagcctgggg tgccataatga atgagctaac tcacattaat 660
 tgcgttgcgc tcactgcccq ctttccaatc nggaaactgt cgtgccaact gcattaatga 720
 atcggccaac ggcggggaa aagcggttg cgtattggc gctttccgc ttcctcgctc 780
 aatgaatccc tgcgctcngt cttccgntg cggnaacgg tatcactcac tcnaatt 837

<210> 30
 <211> 850
 <212> DNA
 <213> Homo sapiens

<220>
 <223> PCR of human ADNF III cDNA from human
 neuroblastoma, antisense

<400> 30
 atnnatnatca agctatgcat ccaacgcgtt gggagctctc ccatatggtc gacctgcagg 60
 cggccgcact agtgattgct cgttacagat tgtacatatt ttccactttt gagttgagga 120
 agtgttacct gggggaggc ctgtggcagc tgcaagcgtt ttggaactgg actgacctaa 180
 cactctggat gcctgtgact gagagagggg aggagacttt aactggcccg atgagagaga 240
 agaggcatta gcagactgca gggagtatct tgctggtgcc tgggacctct gctctgaccc 300
 aagcccataa gaccttccgt ttccacttgg aagtaactgc tttacagact gagattgtt 360
 aggaatgaa actggcgcgt tgccacccatg acccagtctc attgactgac caacactgta 420
 accctggcct acagatttga ctccatagtt gtttgctgc aggtatccc gcggccatgg 480
 cggccggag catgcacgt cggcccaat tcggccataa gtgagtcgta ttacaattca 540
 ctggccgtcg tttacaacg tcgtgactgg gaaaaccctg gcgttaccca acttaatccc 600
 cttgcagcac atcccccttt cgccagctgg cgttaataac gaagaagccc gcacccatcg 660
 cccttcccaa cagttgcgca gcctgaatgg cgaatggacg cgcctgttag cgccatcaa 720
 accccgggg tgggtgggtt acgcccacgtc gtgaccgcta cacttgcac cccctaaccgc 780
 ccgtccctt cccttcttc ctcccttct cggccacgtcc cccgnttcc cgtccaact 840
 ctaaatcggt 850

<210> 31
 <211> 787
 <212> PRT
 <213> Mus musculus

<220>

<223> mouse activity dependent neurotrophic factor III
(ADNF III)

<400> 31

Met Ser Asn Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val
1 5 10 15Gly Gln Ser Tyr Gly Val Gly Gln Ser Val Arg Leu Gly Leu Gly Gly
20 25 30Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu
35 40 45Leu Pro Ser Gly Asn Gly Arg Ser Phe Gly Leu Gly Ala Glu Gln Arg
50 55 60Pro Pro Ala Ala Ala Arg Tyr Ser Leu Gln Thr Ala Asn Thr Ser Leu
65 70 75 80Pro Pro Gly Gln Val Lys Ser Pro Ser Val Ser Gln Ser Gln Ala Ser
85 90 95Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Pro Pro Ala Ala Thr Gly
100 105 110Pro Pro Pro Ser Asn His Cys Ala Thr Gln Lys Trp Lys Ile Cys Thr
115 120 125Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu
130 135 140Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met
145 150 155 160Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu
165 170 175Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser Cys
180 185 190Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala His
195 200 205Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser
210 215 220Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile
225 230 235 240His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser
245 250 255Val Ala Tyr His Ala Gln Asn Asn Ala Pro Val Pro Pro Lys Pro Gln
260 265 270Pro Lys Val Gln Glu Lys Ala Asp Val Pro Val Lys Ser Ser Pro Gln
275 280 285Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu
290 295 300

Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His His
 305 310 315 320

Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu Lys
 325 330 335

Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn
 340 345 350

Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly Val
 355 360 365

Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu
 370 375 380

Asn Gln Ser Pro Gly Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met
 385 390 395 400

Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Glu Glu Asp Ala Asp Ser
 405 410 415

Pro Ser Cys Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu
 420 425 430

Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe
 435 440 445

Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile
 450 455 460

Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser
 465 470 475 480

His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr
 485 490 495

Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val
 500 505 510

Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp
 515 520 525

Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Val Asp Lys Lys His
 530 535 540

Asn Leu Gly Lys Glu Asp Asp Ser Phe Ser Asp Ser Phe Glu His Leu
 545 550 555 560

Glu Glu Glu Ser Asn Gly Ser Gly Ser Pro Phe Asp Pro Val Phe Glu
 565 570 575

Val Glu Pro Lys Ile Pro Ser Asp Asn Leu Glu Glu Pro Val Pro Lys
 580 585 590

Val Ile Pro Glu Gly Ala Leu Glu Ser Glu Lys Leu Asp Gln Lys Glu
 595 600 605

Glu Glu Glu Glu Glu Glu Asp Gly Ser Lys Tyr Glu Thr Ile
 610 615 620

His Leu Thr Glu Glu Pro Ala Lys Leu Met His Asp Ala Ser Asp Ser
 625 630 635 640
 Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro
 645 650 655
 Ser Glu Ser Gly Pro Gly Ser Gln Gln Ile Ser Asp Phe Glu Asp Asn
 660 665 670
 Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser
 675 680 685
 Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Val
 690 695 700
 Gln Asp Asp Thr Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys
 705 710 715 720
 Val Glu Gly Phe Trp Ser Lys Asp Gln Ser Gln Trp Glu Asn Ala Ser
 725 730 735
 Glu Asn Ala Glu Arg Leu Pro Asn Pro Gln Ile Glu Trp Gln Asn Ser
 740 745 750
 Thr Ile Asp Ser Glu Asp Gly Glu Gln Phe Asp Ser Met Thr Asp Gly
 755 760 765
 Val Ala Asp Pro Met His Gly Ser Leu Thr Gly Val Lys Leu Ser Ser
 770 775 780
 Gln Gln Ala
 785

<210> 32
 <211> 781
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human activity dependent neurotrophic factor III
 (ADNF III)

<400> 32
 Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val
 1 5 10 15
 Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly
 20 25 30
 Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu
 35 40 45
 Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg
 50 55 60
 Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser
 65 70 75 80
 Leu Ser Ser Gly His Leu Lys Ser Pro Ser Leu Ser His Ser Gln Ala
 85 90 95

Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr
 100 105 110
 Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys
 115 120 125
 Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe
 130 135 140
 Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile
 145 150 155 160
 Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr
 165 170 175
 Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser
 180 185 190
 Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala
 195 200 205
 His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp
 210 215 220
 Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn
 225 230 235 240
 Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu
 245 250 255
 Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro
 260 265 270
 Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro
 275 280 285
 Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro
 290 295 300
 Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His
 305 310 315 320
 His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu
 325 330 335
 Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser
 340 345 350
 Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly
 355 360 365
 Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg
 370 375 380
 Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln
 385 390 395 400
 Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp
 405 410 415

Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala
 420 425 430
 Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser
 435 440 445
 Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu
 450 455 460
 Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala
 465 470 475 480
 Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys
 485 490 495
 Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys
 500 505 510
 Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His
 515 520 525
 Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys
 530 535 540
 Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Asp Ser Phe Glu Asn
 545 550 555 560
 Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe
 565 570 575
 Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu
 580 585 590
 Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln
 595 600 605
 Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro
 610 615 620
 Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp
 625 630 635 640
 Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly
 645 650 655
 Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro
 660 665 670
 Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser
 675 680 685
 Lys Pro Ala Ala Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln
 690 695 700
 Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser
 705 710 715 720
 Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu
 725 730 735

Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp
740 745 750

Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Thr Glu Pro Met His
755 760 765

Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala
770 775 780

<210> 33

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 33

Gly Gly Asn Ala Pro Val Ser Ile Pro Gln
1 5 10

<210> 34

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 34

Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser
1 5 10

<210> 35

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 35

Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser
1 5 10 15

<210> 36

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF-9 active
peptide adsorbed onto bovine serum albumin (BSA)
as antigen

<400> 36
Ser Ala Leu Leu Arg Ser Ile Pro Ala
1 5

<210> 37
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ADNF
I/PIF1-related sequence

<400> 37
Ile Gln Leu Glu Thr Glu Ile Gln Glu Lys Gln Ile Ile
1 5 10

<210> 38
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cyclophilin
mRNA mimic primer

<400> 38
atggcacagg aggaaagagc aatgcaggca aagacacc 38

<210> 39
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:neuropeptide
cleavage site

<400> 39
Lys Lys Arg Lys
1

<210> 40
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:neuropeptide
cleavage site

<400> 40
Lys Arg Lys Lys
1

<210> 41
 <211> 800
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(800)
 <223> translation of H3' human ADNF III cDNA clone

<400> 41
 Met Val Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly
 1 5 10 15
 Val Asn Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val
 20 25 30
 Lys Ser Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly
 35 40 45
 Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val
 50 55 60
 Lys Gln Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser
 65 70 75 80
 Glu Gln Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn
 85 90 95
 Ala Ser Ser Leu Ser Ser Gly His Leu Lys Ser Pro Ser Leu Ser His
 100 105 110
 Ser Gln Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala
 115 120 125
 Ala Ala Thr Gly Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp
 130 135 140
 Lys Ile Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser
 145 150 155 160
 Val His Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala
 165 170 175
 Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys
 180 185 190
 Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His
 195 200 205
 Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys
 210 215 220
 Met Ala Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro
 225 230 235 240
 Lys Thr Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser
 245 250 255
 His Thr Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala
 260 265 270

Pro Ala Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro
 275 280 285
 Pro Lys Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys
 290 295 300
 Ser Ser Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr
 305 310 315 320
 Leu Cys Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala
 325 330 335
 Leu Ala His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His
 340 345 350
 Pro Val Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val
 355 360 365
 Tyr Thr Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His
 370 375 380
 Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala
 385 390 395 400
 Pro Ser Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr
 405 410 415
 Tyr Glu Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp
 420 425 430
 Asp Ser Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val
 435 440 445
 Val Leu Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala
 450 455 460
 Arg Lys Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr
 465 470 475 480
 Arg Arg Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser
 485 490 495
 Asp Ile Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp
 500 505 510
 Cys Glu Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu
 515 520 525
 Leu Asn Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe
 530 535 540
 Glu Asn His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala
 545 550 555 560
 Asp Lys Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser
 565 570 575
 Phe Glu Asn Leu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp
 580 585 590

Pro Val Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu
 595 600 605
 His Val Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys
 610 615 620
 Leu Asp Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr
 625 630 635 640
 Glu Glu Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp
 645 650 655
 Gln Asp Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser
 660 665 670
 Gly Pro Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu
 675 680 685
 Met Lys Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala
 690 695 700
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 Arg Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly
 725 730 735
 Phe Trp Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp
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<220>

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Phe Leu Ser Leu
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1 5

<210> 47
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 <223> translation of H3' human ADNF III cDNA clone

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<210> 48
 <211> 39
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 <213> Homo sapiens

<220>
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 <223> translation of H3' human ADNF III cDNA clone

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Phe Leu Ser Leu Cys Glu Met Ile Gly Gln Met Ser Leu Arg Ser Val
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Lys Leu Ile His Met Val Val
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<210> 49
 <211> 25
 <212> PRT
 <213> Homo sapiens

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 <223> translation of H3' human ADNF III cDNA clone

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Ser Ser Lys Leu
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 <223> an additional mouse activity dependent
 neurotrophic factor III (ADNF III) cDNA clone

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Met	Gly	Leu	Pro	Pro	Arg	Ile	Ser	Ser	Leu	Ala	Ser	Gly	Asn	Val	Arg	
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tcg	ttg	cca	tca	cag	cag	atg	gta	aac	cga	ttg	tca	ata	cca	aag	ccc	96
Ser	Leu	Pro	Ser	Gln	Gln	Met	Val	Asn	Arg	Leu	Ser	Ile	Pro	Lys	Pro	
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aac	tta	aat	tca	acg	gga	gtc	aac	atg	atg	tcc	aat	gtt	cac	ctg	cag	144
Asn	Leu	Asn	Ser	Thr	Gly	Val	Asn	Met	Met	Ser	Asn	Val	His	Leu	Gln	
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caa	aac	aac	tat	gga	gtc	aaa	tct	gtg	ggc	cag	agc	tat	ggt	gtt	ggc	192
Gln	Asn	Asn	Tyr	Gly	Val	Lys	Ser	Val	Gly	Gln	Ser	Tyr	Gly	Val	Gly	
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cag	tca	gtg	agg	ctg	gga	cta	ggt	ggc	aat	gct	cca	gtt	tcc	atc	cct	240
Gln	Ser	Val	Arg	Leu	Gly	Leu	Gly	Gly	Asn	Ala	Pro	Val	Ser	Ile	Pro	
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caa	cag	tct	cag	tcc	gtg	aaa	cag	tta	ctt	cca	agt	ggg	aat	ggg	agg	288
Gln	Gln	Ser	Gln	Ser	Val	Lys	Gln	Leu	Leu	Pro	Ser	Gly	Asn	Gly	Arg	
85							90						95			
tct	ttt	ggg	cta	ggt	gct	gag	cag	agg	ccc	cca	gca	gca	gcc	agg	tac	336
Ser	Phe	Gly	Leu	Gly	Ala	Glu	Gln	Arg	Pro	Pro	Ala	Ala	Ala	Arg	Tyr	
100							105						110			
tcc	ctg	cag	act	gcc	aac	acc	tct	cta	ccc	cca	ggc	caa	gtg	aag	tct	384
Ser	Leu	Gln	Thr	Ala	Asn	Thr	Ser	Leu	Pro	Pro	Gly	Gln	Val	Lys	Ser	
115							120						125			
ccc	tct	gtg	tct	cag	tca	cag	gca	tct	aga	gta	tta	ggt	cag	tcc	agt	432
Pro	Ser	Val	Ser	Gln	Ser	Gln	Ala	Ser	Arg	Val	Leu	Gly	Gln	Ser	Ser	
130							135						140			
tct	aaa	cct	cca	cca	gcc	gcc	aca	ggc	cct	cct	cca	agc	aac	cac	tgt	480
Ser	Lys	Pro	Pro	Ala	Ala	Thr	Gly	Pro	Pro	Pro	Ser	Asn	His	Cys		
145							150						155		160	
gcc	act	cag	aag	tgg	aaa	atc	tgt	aca	atc	tgt	aac	gag	ctt	ttc	cct	528
Ala	Thr	Gln	Lys	Trp	Lys	Ile	Cys	Thr	Ile	Cys	Asn	Glu	Leu	Phe	Pro	
165							170						175			
gag	aat	gtc	tat	agc	gtt	cac	ttc	gaa	aag	gag	cat	aaa	gct	gag	aaa	576
Glu	Asn	Val	Tyr	Ser	Val	His	Phe	Glu	Lys	Glu	His	Lys	Ala	Glu	Lys	
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gtc cca gcc gta gct aac tac att atg aaa ata cac aat ttt act agc		624	
Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser			
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aaa tgc ctc tac tgt aat cgc tat ttg cct aca gat acc cta ctc aac		672	
Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn			
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His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe			
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Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His Ile Asp			
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gaa gag atg ggg cct aaa acg gat tct act ttg agc ttt gat ttg aca		816	
Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp Leu Thr			
260	265	270	
ttg caa cag ggc agt cac acc aac att cat ctc ctg gtg acc aca tac		864	
Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr Thr Tyr			
275	280	285	
aac ctg agg gat gcc ccg gct gaa tca gtt gct tac cat gcc caa aat		912	
Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala Gln Asn			
290	295	300	
aat gcc cca gtt cct cca aag cca caa cca aaa gtt cag gaa aaa gca		960	
Asn Ala Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu Lys Ala			
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gat gtc ccg gtt aaa agt tca cct caa gct gca gtg ccc tat aaa aaa		1008	
Asp Val Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr Lys Lys			
325	330	335	
gat gtt ggg aag acc ctt tgc cct ctt tgc ttt tca ata cta aaa gga		1056	
Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu Lys Gly			
340	345	350	
ccc ata tct gat gca ctt gca cat cat tta cga gaa aga cac caa gtt		1104	
Pro Ile Ser Asp Ala Leu Ala His His Leu Arg Glu Arg His Gln Val			
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att cag aca gtt cat ccg gtt gag aaa aag cta act tac aaa tgt atc		1152	
Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys Cys Ile			
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cat tgc ctt ggt gtg tat act agc aac atg aca gcc tca acc atc act		1200	
His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr Ile Thr			
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ctg cat cta gtc cac tgc agg ggt gtt gga aaa acc cag aat ggc cag		1248	
Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln			
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Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Gly Leu Ala			
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Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu Lys Lys	
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Arg Lys Leu Glu Glu Asp Ala Asp Ser Pro Ser Cys Phe Glu Glu Lys	
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cca gaa gag cct gtt tta gct tta gac ccc aag ggt cat gaa gat	1440
Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His Glu Asp	
465 470 475 480	
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Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe Asn Lys	
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Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala Ser Leu	
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Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys Arg Lys	
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aag tgt gtc cgc gac tgt gaa aag tac aag cct ggt gtg ctg cta ggt	1632
Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu Leu Gly	
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Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp Phe Asp	
545 550 555 560	
gct gag tgg ctg ttt gaa aat cac gat gag aaa gac tca aga gtc aat	1728
Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg Val Asn	
565 570 575	
gct agc aag act gtt gac aaa aag cat aac ctt ggg aaa gaa gat gat	1776
Ala Ser Lys Thr Val Asp Lys Lys His Asn Leu Gly Lys Glu Asp Asp	
580 585 590	
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Ser Phe Ser Asp Ser Phe Glu His Leu Glu Glu Ser Asn Gly Ser	
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Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile Pro Ser	
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625 630 635 640	
gaa tct gag aag cta gac caa aaa gag gag gag gag gag gag gag	1968
Glu Ser Glu Lys Leu Asp Gln Lys Glu Glu Glu Glu Glu Glu Glu	
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Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Ala	
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Lys Leu Met His Asp Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val	
675 680 685	
gtt gag tgg aaa gat ggt gct tca cca tct gag agt ggg cct ggt tcc	2112
Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser	
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caa caa atc tca gac ttt gag gat aat aca tgt gaa atg aaa cca gga	2160
Gln Gln Ile Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly	
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Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys	
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cca gct gcc aaa aaa aag gct aca gtg caa gat gac aca gag cag tta	2256
Pro Ala Ala Lys Lys Ala Thr Val Gln Asp Asp Thr Glu Gln Leu	
740 745 750	
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Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser Lys	
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785 790 795 800	
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Glu His Phe Asp Ser Met Thr Asp Gly Val Ala Asp Pro Met His Gly	
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Gln Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro	
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Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly Arg
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Ser Phe Gly Leu Gly Ala Glu Gln Arg Pro Pro Ala Ala Ala Arg Tyr
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Ser Leu Gln Thr Ala Asn Thr Ser Leu Pro Pro Gly Gln Val Lys Ser
 115 120 125

Pro Ser Val Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln Ser Ser
 130 135 140

Ser Lys Pro Pro Pro Ala Ala Thr Gly Pro Pro Pro Ser Asn His Cys
 145 150 155 160

Ala Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu Phe Pro
 165 170 175

Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala Glu Lys
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Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser
 195 200 205

Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn
 210 215 220

His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe
 225 230 235 240

Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His Ile Asp
 245 250 255

Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp Leu Thr
 260 265 270

Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr Thr Tyr
 275 280 285

Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala Gln Asn
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Asn Ala Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu Lys Ala
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Asp Val Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr Lys Lys
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Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu Lys Gly
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Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys Cys Ile
 370 375 380

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 385 390 395 400

Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln
 405 410 415

Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Gly Leu Ala
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Arg Lys Leu Glu Glu Asp Ala Asp Ser Pro Ser Cys Phe Glu Glu Lys
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Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe Asn Lys
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Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala Ser Leu
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Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Ala
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Lys Leu Met His Asp Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val
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Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser
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Gln Gln Ile Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly
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Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys
 725 730 735

Pro Ala Ala Lys Lys Lys Ala Thr Val Gln Asp Asp Thr Glu Gln Leu
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Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser Lys
 755 760 765

Asp Gln Ser Gln Trp Glu Asn Ala Ser Glu Asn Ala Glu Arg Leu Pro
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Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp Gly
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<210> 56

<211> 2181

<212> DNA

<213> Homo sapiens

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<223> H3 human activity dependent neurotrophic factor
 III (ADNF III) clone

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 Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser Val His Leu
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 Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly Tyr Ser Val
 35 40 45

ggc cag tca atg aga ctg ggt cta ggt ggc aac gca cca gtt tcc att 192
 Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile
 50 55 60

cct caa caa tct cag tct gta aag cag tta ctt cca agt gga aac gga 240
 Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly
 65 70 75 80

agg tct tat ggg ctt ggg tca gag cag agg tcc cag gca cca gca aga 288
 Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala Pro Ala Arg
 85 90 95

tac tcc ctg cag tct gct aat gcc tct tct ctc tca tcg ggc cag tta 336
 Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser Gly Gln Leu
 100 105 110

aag tct cct tcc ctc tct cag tca cag gca tcc aga gtg tta ggt cag	384
Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln	
115 120 125	
tcc agt tcc aaa cct gct gca gct gcc aca ggc cct ccc cca ggt aac	432
Ser Ser Ser Lys Pro Ala Ala Ala Thr Gly Pro Pro Pro Gly Asn	
130 135 140	
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Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu	
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ttt cct gaa aat gtc tat agt gtg cac ttc gaa aaa gaa cat aaa gct	528
Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala	
165 170 175	
gag aaa gtc cca gca gta gcc aac tac att atg aaa ata cac aat ttt	576
Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe	
180 185 190	
act agc aaa tgc ctc tac tgt aat cgc tat tta ccc aca gat act ctg	624
Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu	
195 200 205	
ctc aac cat atg tta att cat ggt ctg tct tgt cca tat tgc cgt tca	672
Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser	
210 215 220	
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Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His	
225 230 235 240	
att gat gaa gag atg gga cct aaa aca gat tct act ttg agt ttt gat	768
Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp	
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ttg aca ttg cag cag ggt agt cac act aac atc cat ctc ctg gta act	816
Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr	
260 265 270	
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Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala	
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Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu	
290 295 300	
aag gca gat atc cct gta aaa agt tca cct caa gct gca gtg ccc tat	960
Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr	
305 310 315 320	
aaa aaa gat gtt ggg aaa acc ctt tgt cct ctt tgc ttt tca atc cta	1008
Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu	
325 330 335	
aaa gga ccc ata tct gat gca ctt gca cat cac tta cga gag agg cac	1056
Lys Gly Pro Ile Ser Asp Ala Leu Ala His His Leu Arg Glu Arg His	
340 345 350	

caa gtt att cag acg gtt cat cca gtt gag aaa aag ctc acc tac aaa	1104
Gln Val Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys	
355 360 365	
tgt atc cat tgc ctt ggt gtg tat acc acg aac atg acc gcc tca act	1152
Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr	
370 375 380	
atc act ctg cat cta gtt cac tgc agg ggc gtt gga aag acc caa aat	1200
Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn	
385 390 395 400	
ggc cag gat aag aca aat gca ccc tct cgg ctt aat cag tct cca agt	1248
Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Ser	
405 410 415	
ctg gca cct gtg aag cgc act tac gag caa atg gaa ttt ccc tta ctg	1296
Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu	
420 425 430	
aaa aaa cga aag tta gat gat gat agt gat tca ccc agc ttc ttt gaa	1344
Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser Phe Phe Glu	
435 440 445	
gag aag cct gaa gag cct gtt gtt gct tta gac ccc aag ggt cat	1392
Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His	
450 455 460	
gaa gat gat tcc tat gaa gcc agg aaa agc ttt cta aca aag tat ttc	1440
Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe	
465 470 475 480	
aac aaa cag ccc tat ccc acc agg aga gaa att gag aag cta gca gcc	1488
Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala	
485 490 495	
agt tta tgg tta tgg aag agt gac atc gct tcc cat ttt agt aac aaa	1536
Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys	
500 505 510	
agg aag aag tgt gtc cgt gat tgt gaa aag tac aag cct ggc gtg ttg	1584
Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu	
515 520 525	
ctg ggg ttt aac atg aaa gaa tta aat aaa gtc aag cat gag atg gat	1632
Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp	
530 535 540	
ttt gat gct gag tgg cta ttt gaa aat cat gat gag aag gat tcc aga	1680
Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg	
545 550 555 560	
gtc aat gct agt aag act gct gac aaa aag ctc aac ctt ggg aag gaa	1728
Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu Gly Lys Glu	
565 570 575	
gat gac agt tcc tca gac agt ttt gaa aat ttg gaa gaa gaa tcc aat	1776
Asp Asp Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu Glu Ser Asn	
580 585 590	

gaa agt ggt agc cct ttt gac cct gtt ttt gaa gtt gaa cct aaa atc	1824
Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile	
595 600 605	
tct aac gat aac cca gag gaa cat gta ctg aag gta att cct gag gat	1872
Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile Pro Glu Asp	
610 615 620	
gct tca gaa tct gag gag aag cta gac caa aaa gag gat ggt tca aaa	1920
Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp Gly Ser Lys	
625 630 635 640	
· tac gaa act att cat ttg act gag gaa cca acc aaa cta atg cac aat	1968
Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu Met His Asn	
645 650 655	
gca tct gat agt gag gtt gac caa gac gat gtt gag tgg aaa gac	2016
Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp	
660 665 670	
ggt gct tct cca tct gag agt ggg cct gga tcc caa caa gtg tca gac	2064
Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser Gln Gln Val Ser Asp	
675 680 685	
ttt gag gac aat acc tgc gaa atg aaa cca gga acc tgg tct gac gag	2112
Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu	
690 695 700	
tct tcc caa agc gaa gat gca agg agc agt aag cca gct gcc aaa aaa	2160
Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys	
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aaa ggc tac cat gca agg tga	2181
Lys Gly Tyr His Ala Arg	
725	

<210> 57

<211> 726

<212> PRT

<213> Homo sapiens

<400> 57

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Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser Val His Leu	
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Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly Tyr Ser Val	
35 40 45	

Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile	
50 55 60	

Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly	
65 70 75 80	

Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala Pro Ala Arg	
85 90 95	

Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser Gly Gln Leu
 100 105 110
 Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln
 115 120 125
 Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr Gly Pro Pro Pro Gly Asn
 130 135 140
 Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu
 145 150 155 160
 Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala
 165 170 175
 Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe
 180 185 190
 Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu
 195 200 205
 Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser
 210 215 220
 Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His
 225 230 235 240
 Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp
 245 250 255
 Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr
 260 265 270
 Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala
 275 280 285
 Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu
 290 295 300
 Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr
 305 310 315 320
 Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu
 325 330 335
 Lys Gly Pro Ile Ser Asp Ala Leu Ala His His Leu Arg Glu Arg His
 340 345 350
 Gln Val Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys
 355 360 365
 Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr
 370 375 380
 Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn
 385 390 395 400
 Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Ser
 405 410 415

Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu
 420 425 430
 Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser Phe Phe Glu
 435 440 445
 Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His
 450 455 460
 Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe
 465 470 475 480
 Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala
 485 490 495
 Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys
 500 505 510
 Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu
 515 520 525
 Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp
 530 535 540
 Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg
 545 550 555 560
 Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu Gly Lys Glu
 565 570 575
 Asp Asp Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu Ser Asn
 580 585 590
 Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile
 595 600 605
 Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile Pro Glu Asp
 610 615 620
 Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp Gly Ser Lys
 625 630 635 640
 Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu Met His Asn
 645 650 655
 Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp
 660 665 670
 Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser Gln Gln Val Ser Asp
 675 680 685
 Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu
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 Lys Gly Tyr His Ala Arg
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 <211> 4193
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<220>
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 III (ADNF III) clone

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 ttctccttaa ttgcccctac tgtaccttca atgcagacaa aaagactttg gaaacacaca 180
 ttaaaatatt tcatgctccg aacgccagcg caccaggtag cagcttcagc actttcaaag 240
 ataaaaccaa aatgatggc cttaaactta agcaggctga cagtgttagag caagctgttt 300
 attactgtaa gaagtgcact taccgagatc ctctttatga aatagttagg aagcacattt 360
 acagggaaaca tttcagcat gtggcagcac cttacatagc aaaggcagga gaaaaatcac 420
 tcaatggggc agtcccctta ggctcgaatg cccgagaaga gagtagtatt cactgcaagc 480
 gatgcctttt c atg cca aag tcc tat gaa gct ttg gta cag cat gtc atc 530
 Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val Ile
 1 5 10
 gaa gac cat gaa cgt ata ggc tat cag gtc act gcc atg att ggg cac 578
 Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly His
 15 20 25
 aca aat gta gtg gtt ccc cga tcc aaa ccc ttg atg cta att gct ccc 626
 Thr Asn Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala Pro
 30 35 40 45
 aaa cct caa gac aag aag agc atg gga ctc cca cca agg atc ggt tcc 674
 Lys Pro Gln Asp Lys Ser Met Gly Leu Pro Pro Arg Ile Gly Ser
 50 55 60
 ctt gct tct gga aat gtc cgg tct tta cca tca cag cag atg gtg aat 722
 Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val Asn
 65 70 75
 cga ctc tca ata cca aag cct aac tta aat tct aca gga gtc aac atg 770
 Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn Met
 80 85 90
 atg tcc agt gtt cat ctg cag cag aac aac tat gga gtc aaa tct gta 818
 Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val
 95 100 105
 ggc cag ggt tac agt gtt ggt cag tca atg aga ctg ggt cta ggt ggc 866
 Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly
 110 115 120 125

aac gca cca gtt tcc att cct caa caa tct cag tct gta aag cag tta	914
Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu	
130 135 140	
ctt cca agt gga aac gga agg tct tat ggg ctt ggg tca gag cag agg	962
Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg	
145 150 155	
tcc cag gca cca gca aga tac tcc ctg cag tct gct aat gcc tct tct	1010
Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser	
160 165 170	
ctc tca tcg ggc cag tta aag tct cct ctc tct cag tca cag gca	1058
Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala	
175 180 185	
tcc aga gtg tta ggt cag tcc agt tcc aaa cct gct gca gct gcc aca	1106
Ser Arg Val Leu Gly Gln Ser Ser Lys Pro Ala Ala Ala Ala Thr	
190 195 200 205	
ggc cct ccc cca ggt aac act tcc tca act caa aag tgg aaa ata tgt	1154
Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys	
210 215 220	
aca atc tgt aat gag ctt ttt cct gaa aat gtc tat agt gtg cac ttc	1202
Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe	
225 230 235	
gaa aaa gaa cat aaa gct gag aaa gtc cca gca gta gcc aac tac att	1250
Glu Lys His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile	
240 245 250	
atg aaa ata cac aat ttt act agc aaa tgc ctc tac tgt aat cgc tat	1298
Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr	
255 260 265	
tta ccc aca gat act ctg ctc aac cat atg tta att cat ggt ctg tct	1346
Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser	
270 275 280 285	
tgt cca tat tgc cgt tca act ttc aat gat gtg gaa aag atg gcc gca	1394
Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala	
290 295 300	
cac atg cgg atg gtt cac att gat gaa gag atg gga cct aaa aca gat	1442
His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp	
305 310 315	
tct act ttg agt ttt gat ttg aca ttg cag cag ggt agt cac act aac	1490
Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn	
320 325 330	
atc cat ctc ctg gta act aca tac aat ctg agg gat gcc cca gct gaa	1538
Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu	
335 340 345	
tct gtt gct tac cat gcc caa aat aat cct cca gtt cct cca aag cca	1586
Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro	
350 355 360 365	

cag cca aag gtt cag gaa aag gca gat atc cct gta aaa agt tca cct		1634
Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro		
370	375	380
caa gct gca gtg ccc tat aaa aaa gat gtt ggg aaa acc ctt tgt cct		1682
Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro		
385	390	395
ctt tgc ttt tca atc cta aaa gga ccc ata tct gat gca ctt gca cat		1730
Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His		
400	405	410
cac tta cga gag agg cac caa gtt att cag acg gtt cat cca gtt gag		1778
His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu		
415	420	425
aaa aag ctc acc tac aaa tgt atc cat tgc ctt ggt gtg tat acc agc		1826
Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser		
430	435	440
445		
aac atg acc gcc tca act atc act ctg cat cta gtt cac tgc agg ggc		1874
Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly		
450	455	460
gtt gga aag acc caa aat ggc cag gat aag aca aat gca ccc tct cgg		1922
Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg		
465	470	475
ctt aat cag tct cca agt ctg gca cct gtg aag cgc act tac gag caa		1970
Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln		
480	485	490
atg gaa ttt ccc tta ctg aaa aaa cga aag tta gat gat gat agt gat		2018
Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp		
495	500	505
tca ccc agc ttc ttt gaa gag aag cct gaa gag cct gtt gtt tta gct		2066
Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala		
510	515	520
525		
tta gac ccc aag ggt cat gaa gat gat tcc tat gaa gcc agg aaa agc		2114
Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser		
530	535	540
ttt cta aca aag tat ttc aac aaa cag ccc tat ccc acc agg aga gaa		2162
Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu		
545	550	555
att gag aag cta gca gcc agt tta tgg tta tgg aag agt gac atc gct		2210
Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala		
560	565	570
tcc cat ttt agt aac aaa agg aag aag tgt gtc cgt gat tgt gaa aag		2258
Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys		
575	580	585
tac aag cct ggc gtg ttg ctg ggg ttt aac atg aaa gaa tta aat aaa		2306
Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys		
590	595	600
605		

gtc aag cat gag atg gat ttt gat gct gag tgg cta ttt gaa aat cat		2354
Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His		
610	615	620
gat gag aag gat tcc aga gtc aat gct agt aag act gct gac aaa aag		2402
Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys		
625	630	635
ctc aac ctt ggg aag gaa gat gac agt tcc tca gac agt ttt gaa aat		2450
Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Asp Ser Phe Glu Asn		
640	645	650
ttg gaa gaa gaa tcc aat gaa agt ggt agc cct ttt gac cct gtt ttt		2498
Leu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe		
655	660	665
gaa gtt gaa cct aaa atc tct aac gat aac cca gaa gaa cat gta ctg		2546
Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu		
670	675	680
685		
aag gta att cct gag gat gct tca gaa tct gag gag aag cta gac caa		2594
Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln		
690	695	700
aaa gaa gat ggt tca aaa tac gaa act att cat ttg act gag gaa cca		2642
Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro		
705	710	715
acc aaa cta atg cac aat gca tct gat agt gag gtt gac caa gac gat		2690
Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp		
720	725	730
gtt gtt gag tgg aaa gac ggt gct tct cca tct gag agt ggg cct gga		2738
Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly		
735	740	745
tcc caa caa gtg tca gac ttt gag gac aat acc tgc gaa atg aaa cca		2786
Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro		
750	755	760
765		
gga acc tgg tct gac gag tct tcc caa agc gaa gat gca agg agc agt		2834
Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser		
770	775	780
aag cca gct gcc aaa aaa aag gct acc atg caa ggt gac aga gag cag		2882
Lys Pro Ala Ala Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln		
785	790	795
ttg aaa tgg aag aat agt tcc tat gga aaa gtt gaa ggg ttt tgg tct		2930
Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser		
800	805	810
aag gac cag tca cag tgg aag aat gca tct gag aat gat gag cgc tta		2978
Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu		
815	820	825
tct aac ccc cag att gag tgg cag aat agc aca att gac agt gag gat		3026
Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp		
830	835	840
845		

ggg gaa cag ttt gac aac atg act gat gga gta gct gag ccc atg cat	3074																																												
Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met His																																													
850	855	860		ggc agc tta gcc gga gtt aaa ctg agc agc caa cag gcc taagtgccag	3123	Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala		865	870	gttccctggc attggtgaca tgctgcagcc tggaactctg atctccagtg tgactgcaaa	3183	gctgtcttct cactggtaact gccttggag tactggttgg actgtggggc atgtggccgc	3243	tgcagttcca gtggttattt ctaagtctat gacaggacag gctgttcttg cttcagaacc	3303	ttctctgaca gacacggtaa ctaaatgtga aaaaccaata agctggtgac tcatgaatac	3363	acacgagaa aagcagaggt ttattttatc tgccctttca acatttctt ccctctgtga	3423	aatgattggc cagatgtctt tgagaagtgt taaactaatt cacatggtag tgtagggcca	3483	acataacaagc taccagtcta atgtgtatacg tagactttgg gaaaagcgcat tttttttcat	3543	gtattcattc tgaatagttt aaatgtatat ttgtacagtc ttttagacct attcaagtga	3603	tgctcatgat cctgttactg tgtgcccattc atagatttct ttttttagtg ttgcccttgc	3663	tgtgtataaa acgctctatc tagtttacct agcaaaagct caaaactgcg ctagtatgga	3723	ctttttggac agacttagtt ttgcacata accttgcata atcttgcac agaggccagc	3783	cacgtaagat atatatctgg actctcttgg attataggat ttttcttggc ctgaatatcc	3843	ttgacattac agctgtcaaa aacaaaaact ggtatttcag atctgttttc taaaatctt	3903	taagctaaaa tcacatgcaa gaattgactt tgcaactact aatttgaca ctttttagat	3963	ctgtataaaa gtgtgttggc ttgaaggcgc aaaccaatga gtgctgcatt ttggatattt	4023	agttttatct ttagttcaac accatcatgg tggattcatt tataccatct aatatatgac	4083	acactgttgt agtatgtata atttgtgtat ctttattttc cttttgtatt cattttaagc	4143	atctaaataaa attgctgtat tggcttaat gtaaaaaaaaaaaaaaaaaaaaaaaa	4193
860																																													
ggc agc tta gcc gga gtt aaa ctg agc agc caa cag gcc taagtgccag	3123																																												
Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala																																													
865	870																																												
gttccctggc attggtgaca tgctgcagcc tggaactctg atctccagtg tgactgcaaa	3183																																												
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acactgttgt agtatgtata atttgtgtat ctttattttc cttttgtatt cattttaagc	4143																																												
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<210> 59
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 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val Ile Glu Asp His
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Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly His Thr Asn Val
 20 25 30

Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala Pro Lys Pro Gln
 35 40 45

Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly Ser Leu Ala Ser
 50 55 60

Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser
 65 70 75 80

Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser
 85 90 95

Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly
 100 105 110

Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro
 115 120 125

Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser
 130 135 140

Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala
 145 150 155 160

Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser
 165 170 175

Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val
 180 185 190

Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr Gly Pro Pro
 195 200 205

Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys
 210 215 220

Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu
 225 230 235 240

His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile
 245 250 255

His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr
 260 265 270

Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr
 275 280 285

Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg
 290 295 300

Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu
 305 310 315 320

Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu
 325 330 335

Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala
 340 345 350

Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys
 355 360 365

Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln Ala Ala
 370 375 380

Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe
 385 390 395 400

Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His His Leu Arg
 405 410 415

Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu Lys Lys Leu
 420 425 430

Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr
 435 440 445

Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys
 450 455 460

Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln
 465 470 475 480

Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe
 485 490 495

Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser
 500 505 510

Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro
 515 520 525

Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr
 530 535 540

Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys
 545 550 555 560

Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe
 565 570 575

Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro
 580 585 590

Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His
 595 600 605

Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys
 610 615 620

Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu
 625 630 635 640

Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu
 645 650 655

Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu
 660 665 670

Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile
 675 680 685

Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp
 690 695 700

Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu
 705 710 715 720

Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu
 725 730 735

Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser Gln Gln
 740 745 750

Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp
 755 760 765

Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala
 770 775 780

Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln Leu Lys Trp
 785 790 795 800

Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser Lys Asp Gln
 805 810 815

Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu Ser Asn Pro
 820 825 830

Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp Gly Glu Gln
 835 840 845

Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met His Gly Ser Leu
 850 855 860

Ala Gly Val Lys Leu Ser Ser Gln Gln Ala
 865 870

<210> 60

<211> 482

<212> DNA

<213> *Mus musculus*

<220>

<221> promoter

<222> (1)..(482)

<223> mouse activity dependent neurotrophic factor III
 (ADNF III) promoter

<400> 60

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tgcattgcaa cagtgtcacc tgtgagttcc tgtgtctgaa gccgagaaga tccacaaaaat 120

gaggcttttc catagtttgtt ttgtgtttt aacaagaaaa tggagaggct ttttgggtgt 180

ttttgttttt gtttttttgc ctctgacttc tctctgaaac cagccaacaa gtacaactag 240

caatttttaa agattttagca agaacttgca ctgagtttc atttacagga gcacaaaataa 300

aaatatttga ttcaaaaatg catctgagtt cttttaattt ttcctgcagg agaaacctct 360

aaaagtatt gccttcaga gtttctggga atgcctgggg gaggagcctg gaacttgtaa 420
 ctgcttgcct tgagtggcct tctcaactctg gtttctgttc tgttttgttt cgtttggttt 480
 tt 482

<210> 61
 <211> 50
 <212> DNA
 <213> Homo sapiens

<220>
 <223> H6, H7 and H2 clone human activity dependent
 neurotrophic factor III (ADNF III) polymorphic
 region

<220>
 <221> variation
 <222> (47)
 <223> polymorphic site a -> g transition

<400> 61
 gagttaaact gagcagccaa caggcctaag tgccaggttc cctggcattg 50

<210> 62
 <211> 50
 <212> DNA
 <213> Homo sapiens

<220>
 <223> H10 clone human activity dependent neurotrophic
 factor III (ADNF III) polymorphic region

<220>
 <221> modified_base
 <222> (13)
 <223> n = unknown

<220>
 <221> modified_base
 <222> (16)
 <223> n = unknown

<220>
 <221> modified_base
 <222> (20)
 <223> n = unknown

<220>
 <221> modified_base
 <222> (40)
 <223> n = unknown

<220>
 <221> variation
 <222> (47)
 <223> polymorphic site a -> g transition

<400> 62
gagttaaact gancanccan caggcctaag tgccaggttn cctggcgttg 50

<210> 63
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<223> H3, H12 and H4 clone human activity dependent
neurotrophic factor III (ADNF III) polymorphic
region

<220>
<221> variation
<222> ()
<223> polymorphic site a -> g transition

<400> 63
gagttaaact gagcagccaa caggcctaag tgccaggttc cctggcgttg 50